

REMARKS

Reconsideration is requested.

Clams 63-70 are pending. Claims 64-66 and 70 have been withdrawn from consideration.

Paper No. 18 states that "The petition under Rule 181 filed on 04/17/2003 has been acknowledged. The application will be sent back to the special program of the Technical Center for decision on petition after the office action is mailed out." See, page 2 of Paper No. 18. To date, the applicants have not received a Decision on the Petition which was filed more than a year ago. The Office Action (Paper No. 18) is incomplete in not having including a Decision on the applicants Petition. The Examiner's issuance of Paper No. 18 without prior consideration of the applicants Petition is potentially prejudicial to the applicants and, with due respect, inappropriate as the Office has denied the applicants the opportunity to be heard on a petitionable matter prior to prosecution being closed by the issuance of a final rejection. The finality of the Office Action (Paper No. 18) should be withdrawn and a further non-final Office Action issued with a Decision on the applicants Petition.

The undersigned's records indicate that upon receipt of Paper No. 18, the undersigned telephoned and left messages for the Examiner and the Examiner's Supervisor requesting a Decision on the applicants Petition as well as a new Office Action in place of Paper No. 18. To date, the undersigned has not received a response from the Examiner or the Examiner's Supervisor or a Decision on the applicants Petition.

The specification has been amended above to revise the Sequence Listing to amend the designations of "Xaa" at positions 85, 108 and 128 of SEQ ID NO:52 to recite "Pro", "Gly", and "Val", respectively. This clarification was only appreciated upon receipt of Paper No. 18 and the Examiner's unfounded suggestion in ¶9 of Paper No. 18 that the applicants had misled the Office. The applicants and the undersigned have not intended to mislead the Patent Office and did not believe they had misled the Patent Office but rather the applicants believe they inadvertently overlooked the nature of the "Xaa" in the amino acid sequence and the unintended inconsistency with the nucleic acid sequence which has been corrected above.

Specifically, the nucleotide sequence of SEQ ID NO:51 includes a "y" at position 255, a "r" at position 324 and a "y" at position 384. A nucleotide base symbol "y" is a designation for "c" or "t" and that the designation "r" stands for "a" or "g". See, attached copy of 37 CFR § 1.822 (1994). The "X" at position 85 of SEQ ID NO:52 should therefore be "Pro" as opposed to "any amino acid". Similarly, the amino acid at positions 108 and 128 of SEQ ID NO:52 should be "Gly" and "Val", respectively.

The amendments to the Sequence Listing in this regard assure that the nucleotide sequence of SEQ ID NO:51 encodes the amino acid sequence of SEQ ID NO:52, as was intended. No new matter has been added. The need for the Amendment has only been appreciated upon receipt of Paper No. 18.

The Examiner's comment in ¶7 of Paper No. 18 that "There is no indication that SEQ ID NO: 138, 155, 174, 190 or 207 is [sic, were] examined and allowed in the claim 4 [of U.S. Patent No. 6,180,768]" is not understood. The Examiner is urged to appreciate that claim 4 of U.S. Patent No. 6,180,768 claims, among other things, in

subparagraph (ii), a part of SEQ ID NO:52, which is recited in subparagraph (i). SEQ ID NOs: 138, 155, 174, 190 and 207 are fragments of amino acid SEQ ID NO:52; as demonstrated in the following underlined portions of SEQ ID NO:52.

SEQ ID NO:51 (where: y of base 255 is c; r of base 324 is g; and y of base 384 is c)
gacggaatta atttcgcaac agggaattta cctgggtgct ctttctctat cttccttctg 60
gctttgttct catgcttgct tacaccaca gccgggctgg agtaccgtaa tgcctccgga 120
ctctacatgg taactaaca ctgcagtaac ggtagtatcg tgtatgaggc cggggatatt 180
atcctccact tacctggctg tgtccctgc gtacgctctg gcaatacatc aagatgctgg 240
atccctgtga gccccaccgt cgcctgaag tcgacctgcg ccgccaccgc ctctctccgc 300
acgcacgtgg atatgatggg gggggcggcc accctatgct cagctctcta cgtaggagac 360
ctttgtggag cgctatttct tgtcgggcag gggttctcat ggagacatcg ccagcattgg 420
actgtccagg actgcaactg ttccatc

SEQ ID NO:51 (nucleic acids)

SEQ ID NO:52 (Protein wherein residue 85 is Pro, residue 108 is Gly, and residue 128 is Val)

SEQ ID NO:138 Leu Glu Tyr Arg Asn Ala Ser Gly Leu Tyr Met Val

gacggaattaatttcgcaacagggaatttacctgggtgctctttctctatcttcttctg
D G I N F A T G N L P G C S F S I F L L
gctttgttctcatgcttgcttacaccacagccgggctggagtagcctaataatgcctccgga
A L F S C L L T P T A G L E Y R N A S G
ctctacatggtaactaactgactgcagtaacggtagtatcggtgatgaggccggggatatt
L Y M V T N D C S N G S I V Y E A G D I
atcctccacttacctggctgtgtccctgcgtacgctctggcaatacatcaagatgctgg
I L H L P G C V P C V R S G N T S R C W
atccctgtgagccccaccgtcgccgtgaagtcgacctgcgccgccaccgcctctctccgc
I P V S P T V A V K S P C A A T A S L R
acgcacgtggatgatggtggggcggccaccctatgctcagctctctacgtaggagac
T H V D M M V G A A T L C S A L Y V G D
ctttgtggagcgctatttcttgtcgggcaggggttctcatggagacatcgccagcattgg
L C G A L F L V G Q G F S W R H R Q H W
actgtccaggactgcaactgttccatc
T V Q D C N C S I

SEQ ID NO:155 Val Tyr Glu Ala Gly Asp Ile Ile Leu His Leu

gacggaattaatttcgcaacagggaatttacctgggtgctctttctctatcttcttctg
D G I N F A T G N L P G C S F S I F L L
gctttgttctcatgcttgcttacaccacagccgggctggagtagcctaataatgcctccgga
A L F S C L L T P T A G L E Y R N A S G
ctctacatggtaactaactgactgcagtaacggtagtatcggtgatgaggccggggatatt
L Y M V T N D C S N G S I V Y E A G D I
atcctccacttacctggctgtgtccctgcgtacgctctggcaatacatcaagatgctgg
I L H L P G C V P C V R S G N T S R C W
atccctgtgagccccaccgtcgccgtgaagtcgacctgcgccgccaccgcctctctccgc

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I P V S P T V A V K S P C A A T A S L R
acgcacgtggatatgatgggtggggcgccaccctatgctcagctctctacgtaggagac
T H V D M M V G A A T L C S A L Y V G D
ctttgtggagcgctattttcttgcgggcaggggttctcatggagacatcgccagcattgg
L C G A L F L V G Q G F S W R H R Q H W
actgtccaggactgcaactgttccatc
T V Q D C N C S I

SEQ ID NO:174 Val Arg Ser Gly Asn Thr Ser Arg Cys Trp Ile Pro Val

gacggaattaatttcgcaacaggggaatttacctgggttgccttttctctatcttcttctg
D G I N F A T G N L P G C S F S I F L L
gctttgttctcatgcttgcttacacccacagccgggctggagtaccgtaatgcctccgga
A L F S C L L T P T A G L E Y R N A S G
ctctacatggtaactaacgactgcagtaacggtagtatcggtgatgaggccggggatatt
L Y M V T N D C S N G S I V Y E A G D I
atcctccacttacctggctgtgtcccctgcgtacgctctggcaatacatcaagatgctgg
I L H L P G C V P C V R S G N T S R C W
atccctgtgagccccaccgtcgccgtgaagtcgccctgcgcgccaccgcctctctccgc
I P V S P T V A V K S P C A A T A S L R
acgcacgtggatatgatgggtggggcgccaccctatgctcagctctctacgtaggagac
T H V D M M V G A A T L C S A L Y V G D
ctttgtggagcgctattttcttgcgggcaggggttctcatggagacatcgccagcattgg
L C G A L F L V G Q G F S W R H R Q H W
actgtccaggactgcaactgttccatc
T V Q D C N C S I

SEQ ID NO:190 Val Lys Ser Pro Cys Ala Ala Thr Ala Ser

gacggaattaatttcgcaacaggggaatttacctgggttgccttttctctatcttcttctg
D G I N F A T G N L P G C S F S I F L L
gctttgttctcatgcttgcttacacccacagccgggctggagtaccgtaatgcctccgga
A L F S C L L T P T A G L E Y R N A S G
ctctacatggtaactaacgactgcagtaacggtagtatcggtgatgaggccggggatatt
L Y M V T N D C S N G S I V Y E A G D I
atcctccacttacctggctgtgtcccctgcgtacgctctggcaatacatcaagatgctgg
I L H L P G C V P C V R S G N T S R C W
atccctgtgagccccaccgtcgccgtgaagtcgccctgcgcgccaccgcctctctccgc
I P V S P T V A V K S P C A A T A S L R
acgcacgtggatatgatgggtggggcgccaccctatgctcagctctctacgtaggagac
T H V D M M V G A A T L C S A L Y V G D
ctttgtggagcgctattttcttgcgggcaggggttctcatggagacatcgccagcattgg
L C G A L F L V G Q G F S W R H R Q H W
actgtccaggactgcaactgttccatc
T V Q D C N C S I

207 Arg His Arg Gln His Trp Thr Val Gln Asp

gacggaattaatttcgcaacaggggaatttacctgggttgccttttctctatcttcttctg
D G I N F A T G N L P G C S F S I F L L
gctttgttctcatgcttgcttacacccacagccgggctggagtaccgtaatgcctccgga
A L F S C L L T P T A G L E Y R N A S G
ctctacatggtaactaacgactgcagtaacggtagtatcggtgatgaggccggggatatt
L Y M V T N D C S N G S I V Y E A G D I
atcctccacttacctggctgtgtcccctgcgtacgctctggcaatacatcaagatgctgg
I L H L P G C V P C V R S G N T S R C W
atccctgtgagccccaccgtcgccgtgaagtcgccctgcgcgccaccgcctctctccgc
I P V S P T V A V K S P C A A T A S L R

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acgcacgtggatatgatgggtggggggcgccaccctatgctcagctctctacgtaggagac
T H V D M M V G A A T L C S A L Y V G D
ctttgtggagcgcctatttcttgcgggcaggggttctcatggagacatcggcagcattgg
L C G A L F L V G Q G F S W R H R Q H W
actgtccaggactgcaactgttccatc
T V Q D C N C S I
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As for the Examiner's comment in ¶8 of Paper No. 18 and the "sequence analysis date" attached to Paper No. 18, the analysis indicates that amino acids 85, 108 and 128 are "****" which would presumably be any amino acid, or "X", as shown in the unamended Sequence Listing. As established above however, "y" or "r" in the third position of the codon will define only a single amino acid in the noted positions, such that SEQ ID NO:51 encodes SEQ ID NO:52. The search of claim 63 would necessarily require the search of claim 65.

The Examiner's comment in paragraph 7 on page 3 of Paper No. 18 is incorrect to the extent that Serial No. 08/836,075 is asserted to be "under reexamination." Moreover, as noted above with regard to paragraph 6 on page 3 of Paper No. 18, SEQ ID NOs:138, 155, 174, 190 and 207 would have been retrieved in any search of claim 4 of U.S. Patent No. 6,180,768, as part (ii) of claim 4 of U.S. Patent No. 6,180,768, includes part of a polynucleic acid sequence encoding the amino acid sequence of SEQ ID NO:52 which are unique to new HCV type 10.

Further, attached hereto is a Figure 1 compiling and indicating all sequences, with an indication where SEQ ID NOs: 138, 155, 174, 190 and 207 are recited (as type 10-specific) in the specification. Double underlined are the amino acids as recited in claim 64.

Moreover, Table 5 of the specification points out from which genotype the SEQ ID NOs are derived and also the relation between the nucleic acid and amino acid

sequences. SEQ ID NO:1 for instance is a type 1d nucleic acid sequence (Page 52) encoding the amino acid sequence of SEQ ID NO:2 (Page 53). The numbering of the individual nucleotides/amino acids can be retrieved from the sequence alignments in Figure 1 (nt; starting at page 10/74 for SEQ ID NO:51) and Figure 2 (aa; starting at page 24/74 for SEQ ID NO:52), respectively. From Figure 2 it can also be derived that the claimed type 10-specific sequences (of claim 65) are indeed unique.

The Examiner's comment in paragraph 9 of Paper No. 18 has been addressed above. The Examiner has commented that claim 65 is rejoined with claim 63 because they are directed to different DNA molecules is not understood as apparently the Examiner meant to say claim 65 is not rejoined with claim 63. This apparent error is a further basis for requesting a new non-final Office Action as the comment is inconsistent with page 1 of Paper No. 18.

With regard to paragraph 12 on page 4 of Paper No. 18, the relevance of the Examiner's comments is not understood. The fragments of SEQ ID NOs:138, 155, 174, 190 and 207 may be contained in sequences similar to SEQ ID NO:52 but not necessarily the same as SEQ ID NO:52. Results of the nucleic acid sequence search of claim 63 would necessarily reveal sequences of claim 65, even if claim 65 is interpreted broadly. With regard to the Examiner's comments in paragraph 14 of Paper No. 18, the amino acids designated in claim 64 of the pending case are necessarily amino acids which would be encoded by a hepatic C virus polynucleic acid having a nucleotide sequence which is unique to new HCV type 10, as recited in claim 1 of U.S. Patent No. 6,180,768 and discussed above.

The Examiner has restated the restriction requirement in paragraph 15 spanning pages 4-5 of Paper No. 18. The applicants timely petitioned the finality of the restriction requirement and a Decision on the Petition and a new non-final Office Action are requested for the reasons noted above.

The claims have been amended to further distinguish over Hotta et al, sequence accession number D30046, which has been indicated as having been considered by the Examiner in the initialed PTO-1449 Form dated March 3, 2003 ("Database Genbank 'Online! Accession No. D26387, 4 February 1994 (1994-02-04) HOTTA et al: Subtype Analysis of Hepatitis C' Virus in Indonesia" XP002017146 *abstract* and J. CLIN. MICROBIOL., Vol. 32, 1994, pages 3049-3052.") a further copy of which is attached. Attached as Figure 2 (2 pages) is a comparison of SEQ ID NOs: 51 and 52 (designated "51" and "52" in the attached Figure 2) and the sequences of Hotta ("HOTTA '046").

This sequence comparison, like all papers filed by the applicants and the undersigned, was prepared with diligence and care and is believed to be correct however the Examiner is requested to perform the comparison as well to insure the accuracy of the same. Reverse type text (i.e., white letters on black background) in the Hotta sequences of Figure 2 highlight differences between the sequences of the present invention and the sequences of Hotta. Reverse type text (i.e., white letters on a black background) in the amino acid sequence of the present application (i.e., SEQ ID NO:52 or "52") highlight the L186, G217, C252, A254, G290, W293 and H295 amino acids of claim 64.

The grey shaded portion of the sequence of Hotta in page 1 of 2 of Figure 2 is a contiguous 56 base sequence of Hotta which is the same as a portion of the sequence

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of SEQ ID NO:51. Claim 63 has been amended, based on the disclosure of page 8, lines 1-4 of the specification, to further define over Hotta.

Claim 64 has been amended to require the inclusion of at least one of G217 and C252, to further define over Hotta.

The above amendments do not raise new issues requiring further consideration and/or search as Hotta has been previously considered by the Examiner and is of record. Entry of the amendments are requested.

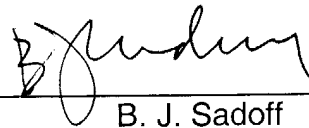
The Section 112, second paragraph, rejection of claims 63 and 67-69 is obviated by the above amendments.

The claims are submitted to be in condition for allowance however a new non-final Office Action and Decision on the applicants Petition are requested, as noted above.

Respectfully submitted,

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